

QY 361 PLASIDRLV-----NYDRLRVNYDRLRVNYDRLRV 392
 DB 359 PLATIDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRV 418
 QY 393 YDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRV 437
 DB 419 YDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRV 463

RESULT 2

025366 PRELIMINARY; PRT; 476 AA.
 ID 025366
 AC 025366
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Pucosyltransferase.
 GN OrderedlocusNames=HP0651;
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteraceae; Helicobacter.
 OC NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
 RA Tomb J.-F., White O., Kervilange A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S.R.,
 RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
 RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
 RA Glodek A., McInerney K., Fitzgerald L.M., Lee N., Adams M.D.,
 RA Hickey E.K., Berg D.B., Gocayne J.D., Uterback T.R., Peterson J.D.,
 RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
 RA Wathey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
 RA Smith H.O., Fraser C.M., Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 pylori."
 RL Nature 388:539-547(1997).
 DR EMBL; AB000578; AAD07710.1; -
 DR PIR; C64601; C64601.
 DR TIGR; HP0651; -
 DR GO; GO:0016757; P:transferase activity, transferring glycosyl. .; IBA.
 DR KW Complete proteome; Glycosyltransferase; Transferase.
 SQ SEQUENCE 476 AA; 55926 MW; 328FDBD36B1F74 CRC64;

Query Match 86.2%; Score 2058.5; DB 2; Length 476;
 Best Local Similarity 84.5%; Pred. No. 7.3e-130;
 Matches 394; Conservative 13; Mismatches 28; Indels 31; Gaps 3;

QY 1 MFQPLDADYVESASIEKMAKSKS-PPPLKIAVANMWDGDEIKKPKSVLYPIFSORITIAL 59
 DB 1 MFQPLDADYVESASIEKMAKSKSPPPLKIAVANMWDGDEIKKPKSVLYPIFSORITIAL 60
 QY 60 HONPNEFSDLVFNSPLGSAKILSYONAKRVYTGNEVEPNFNLFDYAIIGDELDPRDRY 119
 DB 61 HONPNEFSDLVFNSPLGSAKILSYONAKRVYTGNEVEPNFNLFDYAIIGDELDPRDRY 120
 QY 120 LRMPLYYRLHKKASVNDTTSFYKDKNSLYTLKKPSHQKRNPNICAVVNDSDPLK 179
 DB 121 LRMPLYYRLHKKASVNDTTSFYKDKNSLYTLKKPSHQKRNPNICAVVNDSDPLK 180
 QY 180 RGVVSFVANSNANAPRANAFYDALNSIEPVYGGGSKNTLGYVNGKSEFSLQYKFNLCPE 239
 DB 181 RGVVSFVANSNANAPRANAFYDALNSIEPVYGGGSKNTLGYVNGKSEFSLQYKFNLCPE 240
 QY 240 NSOGYGVYTEKILDAVFSHTIPIYWGSPSYAKDPNPKFVNVHDNNFDBAIDYIKYIAT 299
 DB 241 NSOGYGVYTEKILDAVFSHTIPIYWGSPSYAKDPNPKFVNVHDNNFDBAIDYIKYIAT 300
 QY 300 HPNAYLDMLYENPPLNTLDGKAYFYODLSFKKILDPFKTILNDITVH--NNPFIYRDLH 359
 DB 301 HPNAYLDMLYENPPLNTLDGKAYFYODLSFKKILDPFKTILNDITVH--NNPFIYRDLH 358

QY 360 EPLASI-----DRLRVNYDRLRVNYDRLRVNYDRLRV 391
 DB 359 EPLASIDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRV 418
 QY 392 NYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRV 437
 DB 419 NYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRV 464

RESULT 3

025142 PRELIMINARY; PRT; 425 AA.
 ID 025142
 AC 025142
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Pucosyltransferase.
 GN OrderedlocusNames=HP0379;
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteraceae; Helicobacter.
 OC NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
 RA Tomb J.-F., White O., Kervilange A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S.R.,
 RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
 RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
 RA Glodek A., McInerney K., Fitzgerald L.M., Lee N., Adams M.D.,
 RA Hickey E.K., Berg D.B., Gocayne J.D., Uterback T.R., Peterson J.D.,
 RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
 RA Wathey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
 RA Smith H.O., Fraser C.M., Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 pylori."
 RL Nature 388:539-547(1997).
 DR EMBL; AB000554; AAD07447.1; -
 DR PIR; C64567; C64567.
 DR TIGR; HP0379; -
 DR GO; GO:0016757; P:transferase activity, transferring glycosyl. .; IBA.
 DR KW Complete proteome; Glycosyltransferase; Transferase.
 SQ SEQUENCE 425 AA; 49329 MW; 1182AF180D124A34 CRC64;

Query Match 82.6%; Score 1972.5; DB 2; Length 425;
 Best Local Similarity 85.8%; Pred. No. 3.7e-124;
 Matches 376; Conservative 9; Mismatches 24; Indels 29; Gaps 2;

QY 1 MFQPLDADYVESASIEKMAKSKS-PPPLKIAVANMWDGDEIKKPKSVLYPIFSORITIAL 59
 DB 1 MFQPLDADYVESASIEKMAKSKSPPPLKIAVANMWDGDEIKKPKSVLYPIFSORITIAL 60
 QY 60 HONPNEFSDLVFNSPLGSAKILSYONAKRVYTGNEVEPNFNLFDYAIIGDELDPRDRY 119
 DB 61 HONPNEFSDLVFNSPLGSAKILSYONAKRVYTGNEVEPNFNLFDYAIIGDELDPRDRY 120
 QY 120 LRMPLYYRLHKKASVNDTTSFYKDKNSLYTLKKPSHQKRNPNICAVVNDSDPLK 179
 DB 121 LRMPLYYRLHKKASVNDTTSFYKDKNSLYTLKKPSHQKRNPNICAVVNDSDPLK 180
 QY 180 RGVVSFVANSNANAPRANAFYDALNSIEPVYGGGSKNTLGYVNGKSEFSLQYKFNLCPE 239
 DB 181 RGVVSFVANSNANAPRANAFYDALNSIEPVYGGGSKNTLGYVNGKSEFSLQYKFNLCPE 240
 QY 240 NSOGYGVYTEKILDAVFSHTIPIYWGSPSYAKDPNPKFVNVHDNNFDBAIDYIKYIAT 299
 DB 241 NSOGYGVYTEKILDAVFSHTIPIYWGSPSYAKDPNPKFVNVHDNNFDBAIDYIKYIAT 300
 QY 300 HPNAYLDMLYENPPLNTLDGKAYFYODLSFKKILDPFKTILNDITVH--NNPFIYRDLH 359
 DB 301 HPNAYLDMLYENPPLNTLDGKAYFYODLSFKKILDPFKTILNDITVH--NNPFIYRDLH 360

ALIGNMENTS

RESULT 1

US-10-120-319-1

; Sequence 1, Application US/10120319

; Publication No. US20020164749A1

; GENERAL INFORMATION:

; APPLICANT: Taylor, Diane E.

; APPLICANT: Ge, Zhongming

; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE

; FILE REFERENCE: 07254/049001

; CURRENT APPLICATION NUMBER: US/10/120,319.

; CURRENT FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 464

; TYPE: PRT

; ORGANISM: Helicobacter pylori

US-10-120-319-1

Query Match 87.4%; Score 2086; DB 13; Length 464;

Best Local Similarity 87.4%; Pred. No. 1.2e-165;

Matches 394; Conservative 15; Mismatches 26; Indels 16; Gaps 2;

QY 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWWGDEEIKEFKKSVLYFIPFSORYTIALH 60
 ||||| 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWWGDEEIKEFKNSVLYFILSORYTTITLH 60
 Db 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWWGDEEIKEFKNSVLYFILSORYTTITLH 60

QY 61 QNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGNEVPNPNLFDYAIGFDELDPRDRYL 120
 ||||| 61 QNPNEFSDLVFGNPLGSARKILSYQNAKRVFYTGNEVPNPNLFDYAIGFDELDPRDRYL 120
 Db 61 QNPNEFSDLVFGNPLGSARKILSYQNAKRVFYTGNEVPNPNLFDYAIGFDELDPRDRYL 120

QY 121.RMPLYYDRLHHKAESVNDTTSFYKLKDNSLYTLKKPSHQFKNHPNLCVNVNDESPLKR 180

Tue May 24 08:36:55 2005

pct-us05-01614

Db 121 RMPYYDRLHHKAESVNDTTAPYKLDNSLYALKKPSHCPEKHPNLCVVNDESDPLKR 180
Qy 181 GVVSVFVANSANAPMRNAPYDALNSIEPVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN 240
Db 181 GFASFVASNPNAPIRNAPYDALNSIEPVTGGGSVRNTLGYNVKNKNEFLSQYKFNLCFEN 240
Qy 241 SQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKFVNVDHFNDFDEAIDYIKYLHTH 300
Db 241 TQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKFVNVDHFNDFDEAIDYIKYLHTH 300
Qy 301 PNAYLDMLYENPLNALDGKAYFYQDLSFKKILAPFKTILENDTIYHKSSTSPMWECDLDE 360
Db 301 KNAYLDMLYENPLNTLDGKAYFYQNLSEFKKILAPFKTILENDTIYH--DNPPIFCRDLNE 358
Qy 361 PLASIDDLRV-----NYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRV 406
Db 359 PLVTIDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRV 418
Qy 407 YERLLQNASPILLELSONTSFKIYRKAYQKPI 437
Db 419 YERLLSKATPILLELSONTTSKIYRKAYQKSL 449

RESULT 2
US-10-189-977-1
; Sequence 1, Application US/10189977
; Publication No. US20030166211A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Robert

ORGANISM: Helicobacter pylori
US-10-189-977-7

Query Match 86.8%; Score 2073; DB 14; Length 478;
Best Local Similarity 84.5%; Pred. No. 1.5e-164;
Matches 393; Conservative 15; Mismatches 27; Indels 30; Gaps 2;

QY 1 MFOPLDAYSASIERKASKEPPPLKIAVANWMDGDEIRKFKSVLYIFISQRYTIALH 60
DB 1 MFOPLDAYSASIERKASKEPPPLKIAVANWMDGDEIRKFKSVLYIFISQRYTIALH 60
QY 61 QNNEFSDLVFSGNPLGSAKILSYONAKRVFTTGENEVNPNLPDYAIGFDELDPRDRL 120
DB 61 QNNEFSDLVFSGNPLGSAKILSYONAKRVFTTGENEVNPNLPDYAIGFDELDPRDRL 120
QY 121 RMPLYDRLHKAESVNDTTPPYKDKNSLYTLKKPSHOFKKNHPLCAVNDSDPLKR 180
DB 121 RMPLYDRLHKAESVNDTTPPYKDKNSLYTLKKPSHOFKKNHPLCAVNDSDPLKR 180
QY 181 GVSFVASNANAPMNAFPAALNSIEPVYGGGSVKNLTGYNVKNKSEFLSQYKFNLCFEN 240
DB 181 GVSFVASNANAPMNAFPAALNSIEPVYGGGSVKNLTGYNVKNKSEFLSQYKFNLCFEN 240
QY 241 SGGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHD PNNFDEAIDYIKYLAHT 300
DB 241 SGGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHD PNNFDEAIDYIKYLAHT 300
QY 301 PNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
DB 301 PNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
QY 361 PLASIDDLRV-----NYDRLRVNYDDL RVNYDDL RVN 392
DB 359 PLATIDDLRVNYDDL RVNYDDL RVNYYDDL RVNYYDDL RVNYYDDL RVNYYDDL RVN 418
QY 393 YDRLRVNYDDL RVNYDDL RVNYYDDL RVNYYDDL RVNYYDDL RVNYYDDL RVN 437
DB 419 YDRLRVNYDDL RVNYDDL RVNYYDDL RVNYYDDL RVNYYDDL RVNYYDDL RVN 463

RESULT 7
US-09-733-524-1
; Sequence 1, Application US/09733524
; Patent No. US200200683472A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the University of Alberta, a Canada Corporation
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM
; FILE REFERENCE: 07254/049002
; CURRENT APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,857
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Helicobacter pylori fucosyltransferase
US-09-733-524-1

Query Match 86.8%; Score 2073; DB 9; Length 501;
Best Local Similarity 87.1%; Pred. No. 1.6e-164;
Matches 393; Conservative 15; Mismatches 27; Indels 16; Gaps 2;

QY 1 MFOPLDAYSASIERKASKEPPPLKIAVANWMDGDEIRKFKSVLYIFISQRYTIALH 60
DB 1 MFOPLDAYSASIERKASKEPPPLKIAVANWMDGDEIRKFKSVLYIFISQRYTIALH 60

QY 61 QNNEFSDLVFSGNPLGSAKILSYONAKRVFTTGENEVNPNLPDYAIGFDELDPRDRL 120
DB 61 QNNEFSDLVFSGNPLGSAKILSYONAKRVFTTGENEVNPNLPDYAIGFDELDPRDRL 120
QY 121 RMPLYDRLHKAESVNDTTPPYKDKNSLYTLKKPSHOFKKNHPLCAVNDSDPLKR 180
DB 121 RMPLYDRLHKAESVNDTTPPYKDKNSLYTLKKPSHOFKKNHPLCAVNDSDPLKR 180
QY 181 GVSFVASNANAPMNAFPAALNSIEPVYGGGSVKNLTGYNVKNKSEFLSQYKFNLCFEN 240
DB 181 GVSFVASNANAPMNAFPAALNSIEPVYGGGSVKNLTGYNVKNKSEFLSQYKFNLCFEN 240
QY 241 SGGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHD PNNFDEAIDYIKYLAHT 300
DB 241 SGGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHD PNNFDEAIDYIKYLAHT 300
QY 301 PNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
DB 301 PNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
QY 361 PLASIDDLRV-----NYDRLRVNYDDL RVNYDDL RVNYYDDL RVNYYDDL RVN 406
DB 359 PLATIDDLRVNYDDL RVNYDDL RVNYYDDL RVNYYDDL RVNYYDDL RVNYYDDL RVN 418
QY 407 YERLONASPLLELSONTSFKIYRKAYOKPI 437
DB 419 YERLONASPLLELSONTSFKIYRKAYOKSL 449

RESULT 8
US-10-120-319-8
; Sequence 8, Application US/10120319
; Publication No. US20020164749A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-8

Query Match 86.7%; Score 2070.5; DB 13; Length 454;
Best Local Similarity 86.5%; Pred. No. 2.2e-164;
Matches 384; Conservative 27; Mismatches 24; Indels 9; Gaps 2;

QY 1 MFOPLDAYSASIERKASKEPPPLKIAVANWMDGDEIRKFKSVLYIFISQRYTIALH 60
DB 1 MFOPLDAYSASIERKASKEPPPLKIAVANWMDGDEIRKFKSVLYIFISQRYTIALH 60
QY 61 QNNEFSDLVFSGNPLGSAKILSYONAKRVFTTGENEVNPNLPDYAIGFDELDPRDRL 120
DB 61 QNNEFSDLVFSGNPLGSAKILSYONAKRVFTTGENEVNPNLPDYAIGFDELDPRDRL 120
QY 121 RMPLYDRLHKAESVNDTTPPYKDKNSLYTLKKPSHOFKKNHPLCAVNDSDPLKR 180
DB 121 RMPLYDRLHKAESVNDTTPPYKDKNSLYTLKKPSHOFKKNHPLCAVNDSDPLKR 180
QY 181 GVSFVASNANAPMNAFPAALNSIEPVYGGGSVKNLTGYNVKNKSEFLSQYKFNLCFEN 240
DB 181 GVSFVASNANAPMNAFPAALNSIEPVYGGGSVKNLTGYNVKNKSEFLSQYKFNLCFEN 240